

**CRF Errors Corrected by the STIC Systems Branch**

CL

**Serial Number:** 081249, 671

CRF Processing Date: 06/16/94 *43*  
 Edited by: AE  
 Verified by: [Signature] (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☒ Changed the spelling of a mandatory field (the headings or subheadings), specifically:  
Attorney (Agent) Information:
- ☐ Inserted a space between the last nucleic designator and the nucleic number for sequences: \_\_\_\_\_
- ☐ Deleted page numbers in the text of the sequence listing, which is considered invalid text.
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted non-ASCII "garbage" at the end of files, and other invalid text, such as a secretary's initials.
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☒ Other: Started Applicant names on same line as heading

ENTERED

**\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/249,671DATE: 06/16/94  
TIME: 16:58:10

INPUT SET: S2395.raw

<p>This Raw Listing contains the General Information Section and up to the first 5 pages.</p>
---

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANTS: Hauptmann, R.  
Falkner, E.  
Bodo, G.  
VoÄ, T.  
Maurer- Fogy, I.

ENTERED

(ii) TITLE OF INVENTION: Process for Preparing and Purifying  
alpha-Interferon

(iii) NUMBER OF SEQUENCES: 12

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
(B) STREET: 1100 New York Avenue, Suite 600  
(C) CITY: Washington  
(D) STATE: D.C.  
(E) COUNTRY: U.S.A.  
(F) ZIP: 20005

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: herewith  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Esmond, Robert W. RWE/EG  
(B) REGISTRATION NUMBER: 32,893  
(C) REFERENCE/DOCKET NUMBER: 0652.1350000

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 371-2600  
(B) TELEFAX: (202) 371-2540

## (2) INFORMATION FOR SEQ ID NO: 1:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/249,671DATE: 06/16/94  
TIME: 16:58:15

INPUT SET: S2395.raw

47  
48 (i) SEQUENCE CHARACTERISTICS:  
49 (A) LENGTH: 25 base pairs  
50 (B) TYPE: nucleic acid  
51 (C) STRANDEDNESS: both  
52 (D) TOPOLOGY: unknown  
53  
54 (ii) MOLECULE TYPE: cDNA  
55  
56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
57  
58 CGTCTTCAAG AATTCGAGAT TATCG 25  
59  
60 (2) INFORMATION FOR SEQ ID NO: 2:  
61  
62 (i) SEQUENCE CHARACTERISTICS:  
63 (A) LENGTH: 56 base pairs  
64 (B) TYPE: nucleic acid  
65 (C) STRANDEDNESS: both  
66 (D) TOPOLOGY: unknown  
67  
68 (ii) MOLECULE TYPE: cDNA  
69  
70  
71  
72 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
73  
74 GACTTCAGAA GCTTCTGCAG TTACGATCGT TATCATTCCT TACTTCTTAA ACTTTC 56  
75  
76 (2) INFORMATION FOR SEQ ID NO: 3:  
77  
78 (i) SEQUENCE CHARACTERISTICS:  
79 (A) LENGTH: 35 base pairs  
80 (B) TYPE: nucleic acid  
81 (C) STRANDEDNESS: both  
82 (D) TOPOLOGY: unknown  
83  
84 (ii) MOLECULE TYPE: cDNA  
85  
86  
87  
88 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
89  
90 ATGCCTATGC ATGTGATCTG CCTCAAACCC ACAGC 35  
91  
92 (2) INFORMATION FOR SEQ ID NO: 4:  
93  
94 (i) SEQUENCE CHARACTERISTICS:  
95 (A) LENGTH: 34 base pairs  
96 (B) TYPE: nucleic acid  
97 (C) STRANDEDNESS: both  
98 (D) TOPOLOGY: unknown  
99

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/249,671DATE: 06/16/94  
TIME: 16:58:21

INPUT SET: S2395.raw

100 (ii) MOLECULE TYPE: cDNA

101

102

103

104 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

105

106 GGCAGATCAC ATGCATAGGC ATTTGTAGCA ATAG

34

107

108 (2) INFORMATION FOR SEQ ID NO: 5:

109

110 (i) SEQUENCE CHARACTERISTICS:

111 (A) LENGTH: 165 amino acids

112 (B) TYPE: amino acid

113 (D) TOPOLOGY: linear

114

115 (ii) MOLECULE TYPE: protein

116

117

118

119 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

120

121 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met  
122 1 5 10 15

123

124 Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
125 20 25 30

126

127 Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln  
128 35 40 45

129

130 Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe  
131 50 55 60

132

133 Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu  
134 65 70 75 80

135

136 Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu  
137 85 90 95

138

139 Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys  
140 100 105 110

141

142 Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu  
143 115 120 125

144

145 Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg  
146 130 135 140

147

148 Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser  
149 145 150 155 160

150

151 Leu Arg Ser Lys Glu  
152 165

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/249,671DATE: 06/16/94  
TIME: 16:58:27

INPUT SET: S2395.raw

153  
154 (2) INFORMATION FOR SEQ ID NO: 6:  
155  
156 (i) SEQUENCE CHARACTERISTICS:  
157 (A) LENGTH: 495 base pairs  
158 (B) TYPE: nucleic acid  
159 (C) STRANDEDNESS: both  
160 (D) TOPOLOGY: unknown  
161  
162 (ii) MOLECULE TYPE: cDNA  
163  
164  
165 (ix) FEATURE:  
166 (A) NAME/KEY: CDS  
167 (B) LOCATION: 1..495  
168  
169  
170 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
171  
172 TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG AGG ACC TTG ATG 48  
173 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met  
174 1 5 10 15  
175  
176 CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG AAG GAC 96  
177 Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
178 20 25 30  
179  
180 AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC AAC CAG TTC CAA 144  
181 Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln  
182 35 40 45  
183  
184 AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC CAG CAG ATC TTC 192  
185 Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe  
186 50 55 60  
187  
188 AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG GAT GAG ACC CTC 240  
189 Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu  
190 65 70 75 80  
191  
192 CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA 288  
193 Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu  
194 85 90 95  
195  
196 GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG 336  
197 Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys  
198 100 105 110  
199  
200 GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC 384  
201 Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu  
202 115 120 125  
203  
204 TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT GTC AGA 432  
205 Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

DATE: 06/16/94  
TIME: 16:58:32

INPUT SET: S2395.raw

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206          130          135          140
207
208 GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC TTG CAA GAA AGT 480
209 Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
210 145          150          155          160
211
212 TTA AGA AGT AAG GAA 495
213 Leu Arg Ser Lys Glu
214          165
215
216
217 (2) INFORMATION FOR SEQ ID NO: 7:
218
219 (i) SEQUENCE CHARACTERISTICS:
220 (A) LENGTH: 165 amino acids
221 (B) TYPE: amino acid
222 (D) TOPOLOGY: linear
223
224 (ii) MOLECULE TYPE: protein
225
226 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
227
228 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
229 1          5          10          15
230
231 Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
232          20          25          30
233
234 Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
235          35          40          45
236
237 Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
238          50          55          60
239
240 Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
241          65          70          75          80
242
243 Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
244          85          90          95
245
246 Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
247          100          105          110
248
249 Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
250          115          120          125
251
252 Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
253          130          135          140
254
255 Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
256          145          150          155          160
257
258 Leu Arg Ser Lys Glu

```

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/249,671DATE: 06/16/94  
TIME: 16:58:38

INPUT SET: S2395.raw

## \*\*\*\*\* PREVIOUSLY ERRORED SEQUENCES - EDITED \*\*\*\*\*

60 (2) INFORMATION FOR SEQ ID NO: 2:

61

62 (i) SEQUENCE CHARACTERISTICS:

63 (A) LENGTH: 56 base pairs

64 (B) TYPE: nucleic acid

65 (C) STRANDEDNESS: both

66 (D) TOPOLOGY: unknown

67

68 (ii) MOLECULE TYPE: cDNA

69

70

71

72 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

73

74 GACTTCAGAA GCTTCTGCAG TTACGATCGT TATCATTCTTAA ACTTTC

56

75

154 (2) INFORMATION FOR SEQ ID NO: 6:

155

156 (i) SEQUENCE CHARACTERISTICS:

157 (A) LENGTH: 495 base pairs

158 (B) TYPE: nucleic acid

159 (C) STRANDEDNESS: both

160 (D) TOPOLOGY: unknown

161

162 (ii) MOLECULE TYPE: cDNA

163

164

165 (ix) FEATURE:

166 (A) NAME/KEY: CDS

167 (B) LOCATION: 1..495

168

169

170 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

171

172 TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG AGG ACC TTG ATG 48

173 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met

174 1 5 10 15

175

176 CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG AAG GAC 96

177 Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp

178 20 25 30

179

180 AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC AAC CAG TTC CAA 144

181 Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln

182 35 40 45

183

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/249,671DATE: 06/16/94  
TIME: 16:58:43

INPUT SET: S2395.raw

184	AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC CAG CAG ATC TTC	192
185	Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe	
186	50 55 60	
187		
188	AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG GAT GAG ACC CTC	240
189	Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu	
190	65 70 75 80	
191		
192	CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA	288
193	Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu	
194	85 90 95	
195		
196	GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG	336
197	Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys	
198	100 105 110	
199		
200	GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC	384
201	Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu	
202	115 120 125	
203		
204	TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT GTC AGA	432
205	Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg	
206	130 135 140	
207		
208	GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC TTG CAA GAA AGT	480
209	Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser	
210	145 150 155 160	
211		
212	TTA AGA AGT AAG GAA	495
213	Leu Arg Ser Lys Glu	
214	165	
215		
216		

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261 (2) INFORMATION FOR SEQ ID NO: 8:

262

263 (i) SEQUENCE CHARACTERISTICS:

264 (A) LENGTH: 869 base pairs

265 (B) TYPE: nucleic acid

266 (C) STRANDEDNESS: both

267 (D) TOPOLOGY: unknown

268

269 (ii) MOLECULE TYPE: cDNA

270

271

272

273 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

274

275 GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAATGA CCAACAGCGG 60

276

277 TTGATTGATC AGGTAGAGGG GCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCTGAC 120

278

279 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA 180



RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/249,671DATE: 06/16/94  
TIME: 16:58:49

INPUT SET: S2395.raw

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280
281 AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTACACG CCGAGACTTA TAGTCGCTTT 240
282
283 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTGAGGTG ATTTTATGAA AAAGAATATC 300
284
285 GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT 360
286
287 CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG 420
288
289 AGAATCTCTC TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTC CCAGGAGGAG 480
290
291 TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG 540
292
293 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGAC CCTCCTAGAC 600
294
295 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GATACAGGGG 660
296
297 GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC 720
298
299 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT 780
300
301 GTCAGAGCAG AAATCATGAG ATCTTTTTTCT TTGTCAACAA ACTTGCAAGA AAGTTTAAGA 840
302
303 AGTAAGGAAT GATAACGATC GTAAC TGCA 869
304
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305 (2) INFORMATION FOR SEQ ID NO: 9:

306

307 (i) SEQUENCE CHARACTERISTICS:

308 (A) LENGTH: 1177 base pairs

309 (B) TYPE: nucleic acid

310 (C) STRANDEDNESS: both

311 (D) TOPOLOGY: unknown

312

313 (ii) MOLECULE TYPE: cDNA

314

315

316 (ix) FEATURE:

317 (A) NAME/KEY: CDS

318 (B) LOCATION: 286..873

319 (D) OTHER INFORMATION: /function= "Cytokine"

320 /product= "Interferon-omega1"

321

322 (ix) FEATURE:

323 (A) NAME/KEY: mat\_peptide

324 (B) LOCATION: 355..873

325 (D) OTHER INFORMATION: /function= "Cytokine"

326 /product= "Interferon-omega"

327

328 (ix) FEATURE:

329 (A) NAME/KEY: sig\_peptide

330 (B) LOCATION: 286..354

331 (D) OTHER INFORMATION: /product= "ST II Leader"

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

DATE: 06/16/94  
TIME: 16:58:55

INPUT SET: S2395.raw

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332
333
334      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
335
336      GAATTGGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG      60
337
338      TTGATTGATC AGGTAGAGGG GCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC      120
339
340      GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA      180
341
342      AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTACACGG CCGAGACTTA TAGTCGCTTT      240
343
344      GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTGAGGTG ATTTT ATG AAA AAG      294
345                                     Met Lys Lys
346                                     -23
347
348      AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA      342
349      Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr
350      -20                               -15                               -10                               -5
351
352      AAT GCC TAT GCA TGT GAT CTG CCT CAG AAC CAT GGC CTA CTT AGC AGG      390
353      Asn Ala Tyr Ala Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg
354                               1                               5                               10
355
356      AAC ACC TTG GTG CTT CTG CAC CAA ATG AGG AGA ATC TCC CCT TTC TTG      438
357      Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu
358                               15                               20                               25
359
360      TGT CTC AAG GAC AGA AGA GAC TTC AGG TTC CCC CAG GAG ATG GTA AAA      486
361      Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys
362          30                               35                               40
363
364      GGG AGC CAG TTG CAG AAG GCC CAT GTC ATG TCT GTC CTC CAT GAG ATG      534
365      Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu His Glu Met
366          45                               50                               55                               60
367
368      CTG CAG CAG ATC TTC AGC CTC TTC CAC ACA GAG CGC TCC TCT GCT GCC      582
369      Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala
370                               65                               70                               75
371
372      TGG AAC ATG ACC CTC CTA GAC CAA CTC CAC ACT GGA CTT CAT CAG CAA      630
373      Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln Gln
374                               80                               85                               90
375
376      CTG CAA CAC CTG GAG ACC TGC TTG CTG CAG GTA GTG GGA GAA GGA GAA      678
377      Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly Glu Gly Glu
378          95                               100                               105
379
380      TCT GCT GGG GCA ATT AGC AGC CCT GCA CTG ACC TTG AGG AGG TAC TTC      726
381      Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe
382          110                               115                               120
383
384      CAG GGA ATC CGT GTC TAC CTG AAA GAG AAG AAA TAC AGC GAC TGT GCC      774

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# RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

DATE: 06/16/94  
TIME: 16:59:00

INPUT SET: S2395.raw

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385  Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala
386  125                      130                      135                      140
387
388  TGG GAA GTT GTC AGA ATG GAA ATC ATG AAA TCC TTG TTC TTA TCA ACA      822
389  Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr
390                      145                      150                      155
391
392  AAC ATG CAA GAA AGA CTG AGA AGT AAA GAT AGA GAC CTG GGC TCA TCT      870
393  Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu Gly Ser Ser
394                      160                      165                      170
395
396  TGAAATGATT CTCATTGATT AATTTGCCAT ATAACACTTG CACATGTGAC TCTGGTCAAT      930
397
398  TCAAAAGACT CTTATTTTCGG CTTTAATCAC AGAATTGACT GAATTAGTTC TGCAAATACT      990
399
400  TTGTCGGTAT ATTAAGCCAG TATATGTTAA AAAGACTTAG GTTCAGGGGC ATCAGTCCCT      1050
401
402  AAGATGTTAT TTATTTTTTAC TCATTTATTT ATTCTTACAT TTTATCATAT TTATACTATT      1110
403
404  TATATTCTTA TATAACAAAT GTTTGCCTTT ACATTGTATT AAGATAACAA AACATGTTCA      1170
405
406  GGATCCA
407

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458  (2) INFORMATION FOR SEQ ID NO: 11:
459
460      (i) SEQUENCE CHARACTERISTICS:
461          (A) LENGTH: 879 base pairs
462          (B) TYPE: nucleic acid
463          (C) STRANDEDNESS: both
464          (D) TOPOLOGY: unknown
465
466      (ii) MOLECULE TYPE: cDNA
467
468
469
470      (ix) FEATURE:
471          (A) NAME/KEY: CDS
472          (B) LOCATION: 286..852
473
474      (ix) FEATURE:
475          (A) NAME/KEY: mat_peptide
476          (B) LOCATION: 355..852
477          (D) OTHER INFORMATION: /function= "Cytokine"
478                                  /product= "Interferon-alpha-2c"
479
480      (ix) FEATURE:
481          (A) NAME/KEY: sig_peptide
482          (B) LOCATION: 286..354
483          (D) OTHER INFORMATION: /product= "ST II Leader"
484
485
486      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

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# RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

DATE: 06/16/94  
TIME: 16:59:06

INPUT SET: S2395.raw

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487
488 GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG 60
489
490 TTGATTGATC AGGTAGAGGG GCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCCTGAC 120
491
492 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA 180
493
494 AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTACACGG CCGAGACTTA TAGTCGCTTT 240
495
496 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTGAGGTG ATTTT ATG AAA AAG 294
497 Met Lys Lys
498 -23
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500 AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA 342
501 Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr
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504 AAT GCC TAT GCA TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG 390
505 Asn Ala Tyr Ala Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg
506 1 5 10
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508 AGG ACC TTG ATG CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC 438
509 Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser
510 15 20 25
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512 TGC TTG AAG GAC AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC 486
513 Cys Leu Lys Asp Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly
514 30 35 40
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516 AAC CAG TTC CAA AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC 534
517 Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile
518 45 50 55 60
519
520 CAG CAG ATC TTC AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG 582
521 Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp
522 65 70 75
523
524 GAT GAG ACC CTC CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG 630
525 Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu
526 80 85 90
527
528 AAT GAC CTG GAA GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT 678
529 Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr
530 95 100 105
531
532 CCC CTG ATG AAG GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA 726
533 Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln
534 110 115 120
535
536 AGA ATC ACT CTC TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG 774
537 Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp
538 125 130 135 140
539

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545	Leu Gln Glu Ser Leu Arg Ser Lys Glu	
546	160 165	
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548	GAAGCTTAAT	879
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**SEQUENCE VERIFICATION REPORT**  
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